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RAW SEQUENCE LISTING   DATE: 01/24/2003
PATENT APPLICATION: US/09/830,751   TIME: 13:11:20

Input Set : A:\Uw966171.app
Output Set: N:\CRF4\01242003\I830751.raw

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 3 <110> APPLICANT: Suthers, Patrick F
 4        Cameron, Douglas C.
 6 <120> TITLE OF INVENTION: Production of 3-Hydroxypropionic Acid in Recombinant
 7        Organisms
 9 <130> FILE REFERENCE: 960296.96617
11 <140> CURRENT APPLICATION NUMBER: 09/830,751
12 <141> CURRENT FILING DATE: 2000-08-30
14 <150> PRIOR APPLICATION NUMBER: 60/151,440
15 <151> PRIOR FILING DATE: 1999-08-30
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/23878
18 <151> PRIOR FILING DATE: 2000-08-30
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1529
26 <212> TYPE: DNA
27 <213> ORGANISM: Saccharomyces cerevisiae
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (25)..(1509)
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36                                1               5
38 atc aag ctg ccc aat ggg ttg gaa tat gag caa cca acg ggg ttg ttc      99
39 Ile Lys Leu Pro Asn Gly Leu Glu Tyr Glu Gln Pro Thr Gly Leu Phe
40  10              15              20                      25
42 atc aac aac aag ttt gtt cct tct aaa cag aac aag acc ttc gaa gtc     147
43 Ile Asn Asn Lys Phe Val Pro Ser Lys Gln Asn Lys Thr Phe Glu Val
44              30              35                      40
46 att aac cct tcc acg gaa gaa gaa ata tgt cat att tat gaa ggt aga     195
47 Ile Asn Pro Ser Thr Glu Glu Glu Ile Cys His Ile Tyr Glu Gly Arg
48          45              50                  55
50 gag gac gat gtg gaa gag gcc gtg cag gcc gcc gac cgt gcc ttc tct     243
51 Glu Asp Asp Val Glu Glu Ala Val Gln Ala Ala Asp Arg Ala Phe Ser
52          60              65                  70
54 aat ggg tct tgg aac ggt atc gac cct att gac agg ggt aag gct ttg     291
55 Asn Gly Ser Trp Asn Gly Ile Asp Pro Ile Asp Arg Gly Lys Ala Leu
56      75              80                  85
58 tac agg tta gcc gaa tta att gaa cag gac aag gat gtc att gct tcc     339
59 Tyr Arg Leu Ala Glu Leu Ile Glu Gln Asp Lys Asp Val Ile Ala Ser
60  90              95                  100                 105
62 atc gag act ttg gat aac ggt aaa gct atc tct tcc tcg aga gga gat     387
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63 Ile Glu Thr Leu Asp Asn Gly Lys Ala Ile Ser Ser Ser Arg Gly Asp
64               110                 115                 120
66 gtt gat tta gtc atc aac tat ttg aaa tct tct gct ggc ttt gct gat    435
67 Val Asp Leu Val Ile Asn Tyr Leu Lys Ser Ser Ala Gly Phe Ala Asp
68               125                 130                 135
70 aaa att gat ggt aga atg att gat act ggt aga acc cat ttt tct tac    483
71 Lys Ile Asp Gly Arg Met Ile Asp Thr Gly Arg Thr His Phe Ser Tyr
72           140                 145                 150
74 act aag aga cag cct ttg ggt gtt tgt ggg cag att att cct tgg aat    531
75 Thr Lys Arg Gln Pro Leu Gly Val Cys Gly Gln Ile Ile Pro Trp Asn
76       155                 160                 165
78 ttc cca ctg ttg atg tgg gcc tgg aag att gcc cct gct ttg gtc acc    579
79 Phe Pro Leu Leu Met Trp Ala Trp Lys Ile Ala Pro Ala Leu Val Thr
80 170                 175                 180                 185
82 ggt aac acc gtc gtg ttg aag act gcc gaa tcc acc cca ttg tcc gct    627
83 Gly Asn Thr Val Val Leu Lys Thr Ala Glu Ser Thr Pro Leu Ser Ala
84               190                 195                 200
86 ttg tat gtg tct aaa tac atc cca cag gcg ggt att cca cct ggt gtg    675
87 Leu Tyr Val Ser Lys Tyr Ile Pro Gln Ala Gly Ile Pro Pro Gly Val
88               205                 210                 215
90 atc aac att gta tcc ggg ttt ggt aag att gtg gtt gag gcc att aca    723
91 Ile Asn Ile Val Ser Gly Phe Gly Lys Ile Val Val Glu Ala Ile Thr
92           220                 225                 230
94 aac cat cca aaa atc aaa aag gtt gcc ttc aca ggg tcc acg gct acg    771
95 Asn His Pro Lys Ile Lys Lys Val Ala Phe Thr Gly Ser Thr Ala Thr
96       235                 240                 245
98 ggt aga cac att tac cag tcc gca gcc gca ggc ttg aaa aaa gtg act    819
99 Gly Arg His Ile Tyr Gln Ser Ala Ala Ala Gly Leu Lys Lys Val Thr
100 250                 255                 260                 265
102 ttg gag ctg ggt ggt aaa tca cca aac att gtc ttc gcg gac gcc gag   867
103 Leu Glu Leu Gly Gly Lys Ser Pro Asn Ile Val Phe Ala Asp Ala Glu
104               270                 275                 280
106 ttg aaa aaa gcc gtg caa aac att atc ctt ggt atc tac tac aat tct   915
107 Leu Lys Lys Ala Val Gln Asn Ile Ile Leu Gly Ile Tyr Tyr Asn Ser
108           285                 290                 295
110 ggt gag gtc tgt tgt gcg ggt tca agg gtg tat gtt gaa gaa tct att   963
111 Gly Glu Val Cys Cys Ala Gly Ser Arg Val Tyr Val Glu Glu Ser Ile
112           300                 305                 310
114 tac gac aaa ttc att gaa gag ttc aaa gcc gct tct gaa tcc atc aag   1011
115 Tyr Asp Lys Phe Ile Glu Glu Phe Lys Ala Ala Ser Glu Ser Ile Lys
116       315                 320                 325
118 gtg ggc gac cca ttc gat gaa tct act ttc caa ggt gca caa acc tct   1059
119 Val Gly Asp Pro Phe Asp Glu Ser Thr Phe Gln Gly Ala Gln Thr Ser
120 330                 335                 340                 345
122 caa atg caa cta aac aaa atc ttg aaa tac gtt gac att ggt aag aat   1107
123 Gln Met Gln Leu Asn Lys Ile Leu Lys Tyr Val Asp Ile Gly Lys Asn
124               350                 355                 360
126 gaa ggt gct act ttg att acc ggt ggt gaa aga tta ggt agc aag ggt   1155
127 Glu Gly Ala Thr Leu Ile Thr Gly Gly Glu Arg Leu Gly Ser Lys Gly
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128                365                370                   375
130  tac ttc att aag cca act gtc ttt ggt gac gtt aag gaa gac atg aga      1203
131  Tyr Phe Ile Lys Pro Thr Val Phe Gly Asp Val Lys Glu Asp Met Arg
132            380                385                390
134  att gtc aaa gag gaa atc ttt ggc cct gtt gtc act gta acc aaa ttc      1251
135  Ile Val Lys Glu Glu Ile Phe Gly Pro Val Val Thr Val Thr Lys Phe
136            395                400                405
138  aaa tct gcc gac gaa gtc att aac atg gcg aac gat tct gaa tac ggg      1299
139  Lys Ser Ala Asp Glu Val Ile Asn Met Ala Asn Asp Ser Glu Tyr Gly
140  410                415                420                   425
142  ttg gct gct ggt att cac acc tct aat att aat acc gcc tta aaa gtg      1347
143  Leu Ala Ala Gly Ile His Thr Ser Asn Ile Asn Thr Ala Leu Lys Val
144                430                435                440
146  gct gat aga gtt aat gcg ggt acg gtc tgg ata aac act tat aac gat      1395
147  Ala Asp Arg Val Asn Ala Gly Thr Val Trp Ile Asn Thr Tyr Asn Asp
148            445                450                455
150  ttc cac cac gca gtt cct ttc ggt ggg ttc aat gca tct ggt ttg ggc      1443
151  Phe His His Ala Val Pro Phe Gly Gly Phe Asn Ala Ser Gly Leu Gly
152            460                465                470
154  agg gaa atg tct gtt gat gct tta caa aac tac ttg caa gtt aaa gcg      1491
155  Arg Glu Met Ser Val Asp Ala Leu Gln Asn Tyr Leu Gln Val Lys Ala
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159  Val Arg Ala Lys Leu Asp
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164  <211> LENGTH: 495
165  <212> TYPE: PRT
166  <213> ORGANISM: Saccharomyces cerevisiae
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172  Glu Tyr Glu Gln Pro Thr Gly Leu Phe Ile Asn Asn Lys Phe Val Pro
173            20                25                 30
175  Ser Lys Gln Asn Lys Thr Phe Glu Val Ile Asn Pro Ser Thr Glu Glu
176            35                40                 45
178  Glu Ile Cys His Ile Tyr Glu Gly Arg Glu Asp Asp Val Glu Glu Ala
179       50                55                 60
181  Val Gln Ala Ala Asp Arg Ala Phe Ser Asn Gly Ser Trp Asn Gly Ile
182  65                70                 75                    80
184  Asp Pro Ile Asp Arg Gly Lys Ala Leu Tyr Arg Leu Ala Glu Leu Ile
185                85                90                 95
187  Glu Gln Asp Lys Asp Val Ile Ala Ser Ile Glu Thr Leu Asp Asn Gly
188            100               105                110
190  Lys Ala Ile Ser Ser Ser Arg Gly Asp Val Asp Leu Val Ile Asn Tyr
191       115               120                125
193  Leu Lys Ser Ser Ala Gly Phe Ala Asp Lys Ile Asp Gly Arg Met Ile
194       130               135                140
196  Asp Thr Gly Arg Thr His Phe Ser Tyr Thr Lys Arg Gln Pro Leu Gly
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197 145                150                155                160
199 Val Cys Gly Gln Ile Ile Pro Trp Asn Phe Pro Leu Leu Met Trp Ala
200                165                170                175
202 Trp Lys Ile Ala Pro Ala Leu Val Thr Gly Asn Thr Val Val Leu Lys
203                180                185                190
205 Thr Ala Glu Ser Thr Pro Leu Ser Ala Leu Tyr Val Ser Lys Tyr Ile
206           195                200                205
208 Pro Gln Ala Gly Ile Pro Pro Gly Val Ile Asn Ile Val Ser Gly Phe
209      210                215                220
211 Gly Lys Ile Val Val Glu Ala Ile Thr Asn His Pro Lys Ile Lys Lys
212 225                230                235                240
214 Val Ala Phe Thr Gly Ser Thr Ala Thr Gly Arg His Ile Tyr Gln Ser
215                245                250                255
217 Ala Ala Ala Gly Leu Lys Lys Val Thr Leu Glu Leu Gly Gly Lys Ser
218           260                265                270
220 Pro Asn Ile Val Phe Ala Asp Ala Glu Leu Lys Lys Ala Val Gln Asn
221           275                280                285
223 Ile Ile Leu Gly Ile Tyr Tyr Asn Ser Gly Glu Val Cys Cys Ala Gly
224      290                295                300
226 Ser Arg Val Tyr Val Glu Glu Ser Ile Tyr Asp Lys Phe Ile Glu Glu
227 305                310                315                320
229 Phe Lys Ala Ala Ser Glu Ser Ile Lys Val Gly Asp Pro Phe Asp Glu
230                325                330                335
232 Ser Thr Phe Gln Gly Ala Gln Thr Ser Gln Met Gln Leu Asn Lys Ile
233           340                345                350
235 Leu Lys Tyr Val Asp Ile Gly Lys Asn Glu Gly Ala Thr Leu Ile Thr
236           355                360                365
238 Gly Gly Glu Arg Leu Gly Ser Lys Gly Tyr Phe Ile Lys Pro Thr Val
239      370                375                380
241 Phe Gly Asp Val Lys Glu Asp Met Arg Ile Val Lys Glu Glu Ile Phe
242 385                390                395                400
244 Gly Pro Val Val Thr Val Thr Lys Phe Lys Ser Ala Asp Glu Val Ile
245                405                410                415
247 Asn Met Ala Asn Asp Ser Glu Tyr Gly Leu Ala Ala Gly Ile His Thr
248           420                425                430
250 Ser Asn Ile Asn Thr Ala Leu Lys Val Ala Asp Arg Val Asn Ala Gly
251           435                440                445
253 Thr Val Trp Ile Asn Thr Tyr Asn Asp Phe His His Ala Val Pro Phe
254      450                455                460
256 Gly Gly Phe Asn Ala Ser Gly Leu Gly Arg Glu Met Ser Val Asp Ala
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269 <220> FEATURE:
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279 Ala Pro Asn Gln Gln Pro Glu Val Phe Cys Asn Gln Ile Phe Ile Asn
280             15                  20                  25
282 aat gaa tgg cac gat gcc gtc agc agg aaa aca ttc ccc acc gtc aat   147
283 Asn Glu Trp His Asp Ala Val Ser Arg Lys Thr Phe Pro Thr Val Asn
284             30                  35                  40
286 ccg tcc act gga gag gtc atc tgt cag gta gct gaa ggg gac aag gaa   195
287 Pro Ser Thr Gly Glu Val Ile Cys Gln Val Ala Glu Gly Asp Lys Glu
288             45                  50                  55
290 gat gtg gac aag gca cgt gaa ggc cgc ccg ggc gcc ttc cag ctg ggc   243
291 Asp Val Asp Lys Ala Arg Glu Gly Arg Pro Gly Ala Phe Gln Leu Gly
292     60                  65                  70
294 tca cct tgg cgc cgc atg gac gca tca cac agc ggc cgg ctg ctg aac   291
295 Ser Pro Trp Arg Arg Met Asp Ala Ser His Ser Gly Arg Leu Leu Asn
296 75                  80                  85                  90
298 cgc ctg gcc gat ctg atc gag cgg gac cgg acc tac ctg gcg gcc ttg   339
299 Arg Leu Ala Asp Leu Ile Glu Arg Asp Arg Thr Tyr Leu Ala Ala Leu
300             95                  100                 105
302 gag acc ctg gac aat ggc aag ccc tat gtc atc tcc tac ctg gtg gat   387
303 Glu Thr Leu Asp Asn Gly Lys Pro Tyr Val Ile Ser Tyr Leu Val Asp
304             110                 115                 120
306 ttg gac atg gtc ctc aaa tgt ctc cgg tat tat gcc ggc tgg gct gat   435
307 Leu Asp Met Val Leu Lys Cys Leu Arg Tyr Tyr Ala Gly Trp Ala Asp
308             125                 130                 135
310 aag tac cac ggg aaa acc atc ccc att gac gga gac ttc ttc agc tac   483
311 Lys Tyr His Gly Lys Thr Ile Pro Ile Asp Gly Asp Phe Phe Ser Tyr
312     140                 145                 150
314 aca cgc cat gaa cct gtg ggg gtg tgc ggg cag atc att ccg tgg aat   531
315 Thr Arg His Glu Pro Val Gly Val Cys Gly Gln Ile Ile Pro Trp Asn
316 155                 160                 165                 170
318 ttc ccg ctc ctg atg caa gca tgg aag ctg ggc cca gcc ttg gca act   579
319 Phe Pro Leu Leu Met Gln Ala Trp Lys Leu Gly Pro Ala Leu Ala Thr
320             175                 180                 185
322 gga aac gtg gtt gtg atg aag gta gct gag cag aca ccc ctc acc gcc   627
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324             190                 195                 200
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328         205                 210                 215
330 gtc aac att gtg cct gga ttt ggc ccc acg gct ggg gcc gcc att gcc   723
331 Val Asn Ile Val Pro Gly Phe Gly Pro Thr Ala Gly Ala Ala Ile Ala
332     220                 225                 230
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